

FIG. 1

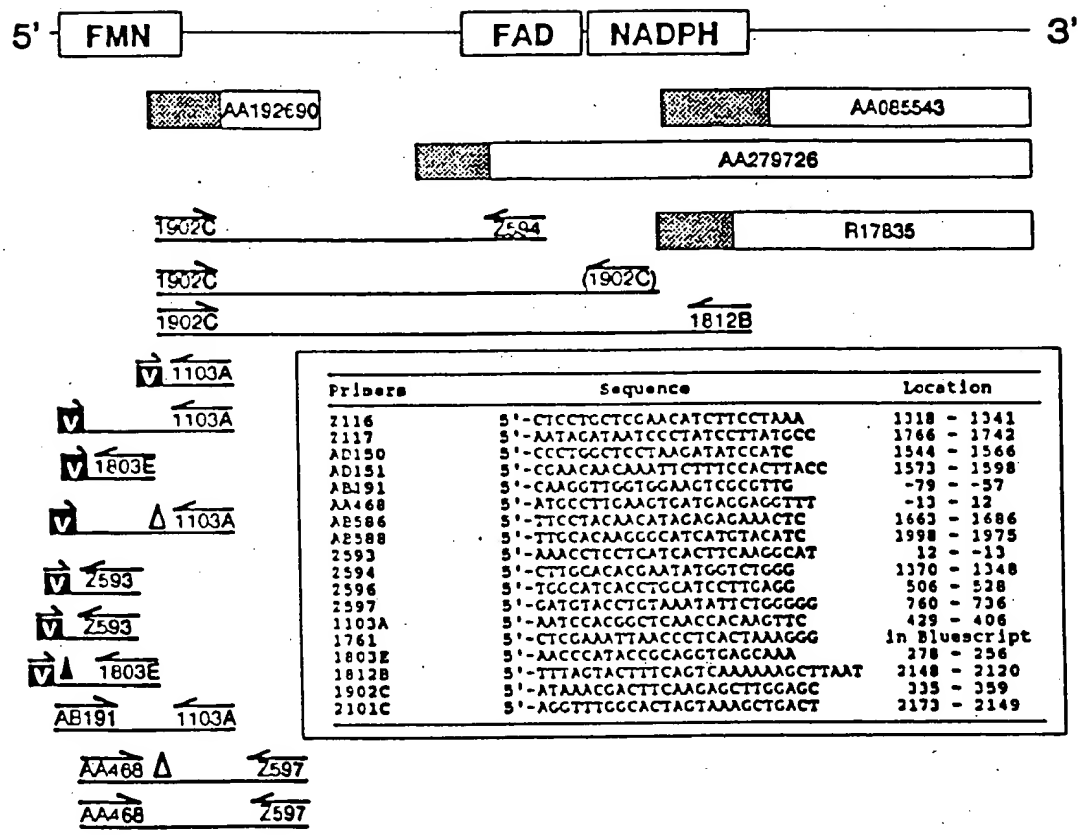


FIG. 2

CAAGGTTGGTGAAGTCCTGTGTCAGGTTCTGTGCCCGGCTGGCGGGTGTTTCTACTGTATACATCCCTTGAAGT

1 ATGAGGAGGTTCTGTACTATATGCTACACAGCAGGACAGGCATCGCAGAAGAAATGTGTGAGCAAGCTGTGGTACATGGATTTCCTGCAGATCTTCAGTGTATTAGTGAA
M R R F L L L Y A T Q G O A K A I A E E H C E O A V V H G F S A D L H C I S E 40

121 TCCGATAAGTATGACCTAAAACCGAACAACAGCTCTCTGTGTGGTTTCTACCACGGGCACCGGAGACCCCGCACACAGCCGCGCAAGTTTGTTAAGGAATAACAGAACCAACA
S D K Y D L K T E T A P L V V V S T T G T G D P P D T A R K F V K E I O N Q T 80

261 CTGCGGTTGATTCTTTGCTCACTCGCGTATGGTTACTGGGTCTCGGTGATTGAGATACACCTACTTTTGAATGGGGGAAGAATAATTGATAACGACTTCAAGAGCTTGGAGCC
L P V D F F A H L R Y G L L G L G D S E Y T Y F C N G G K I I D K R L Q E L G A 120

361 CGGCATTTCTATGACACTGGACATGCAGATGCTGTAGGTTTAGAACTTGTGGTTGACCGTGGAATCTGGCATCTGGCCAGCCCTCAGAAAGCAATTTTAGGTCAAGCAGGACAA
R H F Y D T G H A D D C V G L E L V V E P W I A G L W P A L R K H F R S S R G O 160

481 GAGGAGATAAGTGGGCACCTCCCGGTGGCATCACCTGCATCTTGAGNACAGACCTGTGAAGTCAGAGCTGCTACACATTTGAATCTCAAGTCGAGCTCTCTGAGATTGCGATTCAGGA
E E I S G A L P V A S P A S L R T D L V K S E L L H I E S O V E L L R F D D S G 200

601 AGAAAGGATTCTGAGGTTTTGAAGCAAAATCGAGTGACAGCAACCAATCCAATGTGTAAITGAAGACTTTGAGTCTCACTTACCGTTCGGTACCGTTCACAGCTCTCACAAGCTCTCTG
R K D S E V L K Q N A V N S N O S W V V I E D F E S S L T R S V P P L S O A C T S L 240

721 AATATTCCTGGTTTACCCCGAGAAATTTACAGGTACATCTGCAGGAGTCTCTGGCAGGAGTCTCTGAGATTGGACATTTCAAATACAGACTTTTCTATCAGCTGGAGATGCTGCCCTAACAGT
N I P G L P P E Y L Q V H L Q E S L G Q E E S O V S V T S A D P V F O V P I S K 280

841 GCAGTTCAACTTACTACGAATGATGCCATAAAACCCTCTGCTGGYAGAATTGGACATTTCAAATACAGACTTTTCTATCAGCTGGAGATGCTTCAGGGTGATCTGCCCTAACAGT
A V O L T T N D A I K T T L L V E L D I S N T D F S Y O P G D A F S V I C P N S 320

961 GATTCGAGGTACAAAGCCTACTCCAAGACTGCAGCTTGAGATAAAGAGAGCACTCGCTCTTTGAAAAATAAGGCAGACACAAAGAAAGAGGACTACCTTACCCCCAGCATATA
D S E V Q S L L O R L Q L E D K R E H C V L L K I K A D T K K G A T L P O H I 360

1081 CCTCGGAGTGTCTCTCCAGTTCATTTTACCTGGTGTCTGAATCCGAGCAATCTCAAAGGCATTTTGGCAGCCCTTGGCAGCTATACCAGTGACAGTGTGAAAAAGCGCAGG
P A G C S L Q F I F T W C L E I R A I P K K A F L R A L V D Y T S D S A E K R R 400

1201 CTACAGGAGCTGTGAGTAAACAGGGCAGCGGATTATAGCCGCTTTGTAGCAGATGCTGTGCTCTCTGCTGTGGATCTCTCTCGCTTCCCTCTTGCCAGCCACCACTCAGTCTC
L Q E L C S K O G A A D Y S R F V R D A C A C L L D L L A F P S C O P P L S L 440

1321 CTGCTCGAATCTCTCTAAACTTCAACCCAGACCATATTCGTGCAAGCTCAAGTTTATTCACCCAGAAAGCTCCATTTTGCTCTCAACATTTGGAATTTCTGTCTACTGCCACA
L L E H L P K L O P R P Y S C A S S L F H P G K L H F V F N I V E F L S T A T 480

1441 ACAGAGGTTCTGCGAAGGAGTATGACAGGCTGGCTGGCTGTGGTGGTCTTCAGCCAAACATACATGATCCATCAAGACACAGCGGGAAGCCCTGGCTCTCAAGATA
T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I 520

1561 TCCATCTCTCTCGAACAACAAATCTTCTCCACTTACCAGATGACCCCTCAATCCCCTCAATAAGTGGTGGTCAGAACCGGCATAGCCCGTATTTGGGTTCCTACAACATAGAG
S I S P R T T N S F H L P D P S I P I M V G P G T G I A P F I G F L O H R E 560

1681 AAACCTCAAGAACACACCCAGATGGAAATTTTGAGCAATGTGGTTGTTTTGGCTGCAGCATAAGGATGATTATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGCATGGG
K L Q E O H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G 600

1801 ATCTTAACATCTAAAGGTTTCCCTCTCAAGAGATGCTCTGTTGGGAGGAGGAAGCCCAAGCAAGTATGTAAGACACATCCAGCTTTCAGCCAGCAGGTGGCGAATCCTC
I L T H L K V S F S R D A P V G E E A P A K Y V O D N I O L H G O O V A R I L 640

1921 CTCAGGAGACGGCCATATTTATGTGTGCGAGATGCAAGAATATGCCAAGGATGATACATGTGCCCTTGTGCAAAATAAGCAAGAGGTGGAGTTGAAACATAGAACCAATG
L Q E N G H I Y V C G D A K N M A K D V H D A L V O I I S K E V G V E K L E A M 680

2041 AAAACCTGGCCACTTTAAAGAGAAAAACGCTTACCTTACGGATATTTGGTCTATAAAACCAGAAATTAAGAAAGGATTAAAGCTTTTGTGACTGAAAGTACTAAAGTACGCTTTAC
K T L A T L K E E K R Y L O D I W S *** 698

2161 TAGTGCCAAACCTTTAAATTTTCAAAAGAAAAATTTCTTCAACATTTCTTGAAGGACATGGAGTGGATCATTTTAACAATAACAACAACTTCCTGATTGATTTTACGTAATC
2281 TTCATCTACGCCCTTCTGTGCTGTGACTCTCCCCAAATGGCCGTGTGCTTGAGCTCTTCAGCTTAAAGCGAGCTCTCAGTCCCTACTTAAAGAGCTCTTACTTCCCAAGAACT
2401 TCACAGAGACTGTCTTCCATCGCAAGAGCTTCTGAAATAGGAGACTGACTGAGTACCTCATCTTGTGACTACAGTGCCCACTTAAAGAGTATGAAAGTATGAAATATTATTTA
2521 TATGATGATACCCATTAAGATGCTCATATTAATGACTTAATTAATACATGACTAGACATCTGTATGTATTGTAACATCAAAATGGTTATTTGTTACTAAGCTATATTCTG
2641 ATAAAAATTTTAGGATAATTCCTCAAGGATTTATTTTATGATGCTGGGAATAAGAAATGATTTTAAATTTTCACTCTGGGATATGGATTATCTATCACTACCTACTTTT
2761 TTAAAGTCAAAATTTGAGAAATTTGGGACATTCGATTTCAATTTACAGGTACCCAGTACGATCATTTTAAATAGAAAGATACAACTTTTATTTTCACTCTTTTATTTCTGCTCTT
2881 GGACATTTTGTAGTTTCCCAATATTTGTCTCCATGATACCACTCAAGCAGTGTGGACTTAAATACCTGACTTTAGTATCTTGGATTCTTGGATTATTTAGATTCCCCAGTGTCTAAT
3001 TCCCTGTTAATTTGCAACAACAACAAATATTTGATGAATCTTCTCCACTGTCTTATATATATGTTATTTATGATGCTTGGGATTTAAACATCTCTGTTGAAGGCTTT
3121 TGATCTCTTTGAGAAATAAGATCTGAAGAAATGGCATAATCTTAAAAAAAAAAAAAAA

HsMTRR	
CeMTRR	
HsCPR	MGCSHYDTSSTVSEAVAEVSLFSMTDHLFSLIVGLLTIVFLFRKKKEE	50
HsMTRRFMN.....	24
CeMTRRMRRFLLLTATCCGCAKIAEENCE	24
HsCPR	VFEFTKIGTLTSSVRESSFVEKMKKTGRNIIVFYCSOTGTAEEFANRLSK	100
HsMTRRFMN.....	66
CeMTRR	CAVVVCFSAHLHCISESDK-YDLKT-----ETAPLVVVSTTGTGDP	66
HsCPR	KAELIGLTFRLHALCEHEKTHLNE-----EKLC-AIVVSTGGDAP	66
	DANRYG---MRGMSADPEEYDLADLSSLEIDHALVVFCHATYCEGOPT	146
HsMTRRFMN.....	116
CeMTRR	CTARFVKETCNCTLPVDFFAHLRTGLLGLGDSYTYFCNGGKIIDKRLQ	116
HsCPR	ENCAFFVRRINRNSLENEYLNLDYLLGLGDSYSSYGTIFRKIDKOLT	116
	DNACDFYDLGCTDGD---LSGVKFAVFLGCKTYENFNAWKYVOKRLE	193
HsMTRR	ELCARHFYDICHADDCVGLLVVPEVIAGLVFAIRKHFSSRGCEEISGA	166
CeMTRR	ALCAHRLDRAEADDCVGLLEVEPVIKFFATLASRFDISADKHM---	162
HsCPR	QLGACRFELGLGDDGNLEEDFITVRECFWFAVCENF-----GV	233
HsMTRR	LFVASPAELRTDLVKSELLNIESOVELL--RFDCSGRKDSEVLKNAVNS	214
CeMTRR	-AITESSNLKNCVKTE---EKKALLCKRIEDEESDDEGRGVIGID-	206
HsCPR	EATGEESIKCTEL-----VVHTDIAAKVYNGEMGRKSYEN	271
HsMTRR	NCENVVIEDF---EESLRSVPPLS-CASLNIPLPPEYLOVHLCESLGQ	260
CeMTRR	---MLIFEHTDYPEISLLKGSOTLSHDEHLRVPJAPCFIVSSVSKFLP	253
HsCPR	CKP---FID-----AKNPFLAAVITNRKLN	293
HsMTRR	EEECVS-----VTSADPVFCVPISKAVOLT--NDAIKTLLVELDIS	301
CeMTRR	EDTXLEWCHLCKNFCVVTKFEEVLVVSASFVTDPSKKIKTKRMITVDFG	303
HsCPR	CGTE-----FNLMLHLED	306
HsMTRR	N--TDFSTYFCDAFVVICPNSDSEVOSLLOR-LOLEDKREHCVLLKIKAD	348
CeMTRR	CHAAELCTEFCDAITYCVFPALEVNFIKRCVLDIADOCCEL-SINPK	352
HsCPR	ISCSKIRYESCDHVAVYPANDSALVHOLCK---ILGADLD--VMSLHNL	351
HsMTRR	TKKKGATLPCHIPACCSLOFIFTWGLEIRAIPKAFRLALVDYTSASA	398
CeMTRR	TEKINACIFCHVHKITTLRHMTTCLDIRAPGRPLIRVLAESTSOFNEK	402
HsCPR	DEESKXKF--IFCPTSYRTALTYTLDITNPPRTNVLYELACTASEFSEQ	399
HsMTRR	RPLOEL--CSKCGAACYSRFRVDCACILDLFFAPSCOPPLSLLLEMLP	446
CeMTRR	FRILLEL--CSAGCKHDFDVFRTPLSLADMLFATPNVKKPPVORLIELLP	450
HsCPR	ELLKMHASSGCKELYLSVVVEARRHILAILDCCPSLRPPIDHLCCLLP	449
HsMTRRFAD.....FAD.....FAD.....	496
CeMTRR	RLCPRTYSCASSLHFPGKLFHVFNIVEFLSTATTEVLRKGVCTGWLALL	497
HsCPR	RLCPRTYSSSS---YENRKRLITYSENEFPATGGRHSRKLATDULNSL	496
	RLCARTYSIASSSKVHPNSVNICAVVETETKAGR--INKGVATNUL---	496
HsMTRR	VASVLOPNINASHEDSGKALPKISISPRTTNSFNLP-----DDPSTP	539
CeMTRR	R-----IGDKVOVLCKEFARFLPPLGHTKNSACKLP	529
HsCPR	RAKE-----FVGENCGRALVPHFVRKSOFRLPFK-----ATTP	527
HsMTRRNADPH.....	588
CeMTRR	ITMVCPGTCTIAFFIGLOHREKLOEGHPDGNFGAMW-LFFGCRNKDRYL	579
HsCPR	LLMVCPGTGVSVFLSFLHFLRLKQDPSDFVDVPRVLFEGCRDSSVDAL	574
	VIMVCPGTGVAFVIGFIOERAWLRGCKE---VGETLLTYGCRSDEDYL	574
HsMTRRNADPH.....NADPH.....	638
CeMTRR	FRKELRHFLKNCILTNLKVFSRDPVGEFAFAYTVDNIOLNGCOVAR	621
HsCPR	YHSELEHFVSECIITDLIICESEQ-----XGERVODGLRKYLDKVLPL	618
	YREELAGFHROGALTOLNVAFSRE-----QSHKVYVCHLLKQOREHLWK	618
HsMTRRNADPH.....	687
CeMTRR	ILLQE-NGHITYVCGDAKNHAKDVHDLVOTISKEVGVKLEAMKTLATLK	671
HsCPR	FLTASTESKIFICGDAKNSKDVVQCFSDIVASDQIPDLEAKKLNOLK	666
	LI--EGGAHITYVCGDARNHARDVCHTFTD[VAELEGAMEHQAQVDYIKKLM	666
HsMTRRNADPH/FAD.....	698
CeMTRR	EEKRTLODIWS	682
HsCPR	KSDQYIEDVWG	677
	TKCRYSLDVWS	677

FIG. 4 page 1 of 2

HsMTRR	-----	
CeMTRR	-----	
HsCPR	MGDQVDTSSVTSEAAVEVSLFSMTDMILFSLIVGLLTYWFLPKKKEL	50
	FMN	
HsMTRR	-----MRRFLLLYATOGGAIAEEMCE	24
CeMTRR	-----MTDFLIAFGSQTGOAETIAKSLKE	24
HsCPR	VPEFTKIOTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGAEEFANRLSK	100
	..*.*.*.*.*	
	FMN	
HsMTRR	OAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVSTTGTGDP	66
CeMTRR	KAELIGLTPRLHALDENEKKFNLE-----EKLC-AIVVSTGDDGAP	66
HsCPR	DAHRYG---MRGMSADPEYDLADLSSLPEIDNALVVFCMATYGEDPT	146
	..*.*.*	
	FMN	
HsMTRR	DTARKFVKEIQNQTLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ	116
CeMTRR	DNCARFVRRINRNSELENYLKNLDYVLLGLGDSNYSSYOTIPRKIDKOLT	116
HsCPR	DNAODFYDWLOETDVD---LSGVKFAVFGNGKTYEHFAMGKYVDKRL	193
	..*.*.*	
HsMTRR	ELGARHFYDTGHADDCVGLLEVPEWPIAGLWPAIRKHFSSRGEEISGA	166
CeMTRR	ALGANRFDRAEADDOVGLELEVPEWIEKFATLASRFDISADKMN----	162
HsCPR	OLGAORIFELGLGDDGNLEEDFITVREQFWPAVCEHF-----GV	233
	***..*.*.*.*	
HsMTRR	LPVASPASLRDVLKSELLHIESOVELL--RFDDSGRKDSEVLKONAVNS	214
CeMTRR	-AITESSNLKNOVKTE---EKKALLOKRIEDESDDGRGRVIGID-	206
HsCPR	EATGEESSIROYEL-----VVHTDIDAAKVYMGEMGRKLSYEN	271
	..*.*.*.*	
HsMTRR	NCSNVVIEDF---EESLTRSVPLS-QASLNIPGLPPEYLOVHLOESLGO	260
CeMTRR	---MLIPEHYDYPEISLLKGSOTLSNDENLRVPIAPQPFIVSSVSNRKLP	253
HsCPR	OKP-----PFD-----AKNPFLAAVTINRKLN	293
	..*.*	
HsMTRR	EESQVS-----VTSADPVFCVPISKAVOLTY--NDAIKTLLVELDIS	301
CeMTRR	EDTKLEWNLCKMPGVVTKPFVFLVVSAEFVTDPFSSKIKTKRMITVDFG	303
HsCPR	OGTE-----RHLMLHLELD	306
	..*.*	
HsMTRR	N--TDFSYPGDAFSVICPNSDSEVQSLLOR-LQLEDKREHCVLLKIKAD	348
CeMTRR	DHAAELOEYEPGDAIYFCVPNPALEVNFIKRCGVLDIADOOCEL-SINPK	352
HsCPR	ISDSKIRYESGDHVAVYPANDSALVNOLGK---ILGADLD--VMSLNHL	351
	..*.*.*	
HsMTRR	TKKKGATLPQHIPAGCSLOFIFTWCLEIRAIKKAFLRALVDYTSDSA	398
CeMTRR	TEKINAQIPGHVHKITTLRHMFTICLDIRRAPGRPLIRVLAESTSDPNEK	402
HsCPR	DEESNKKHP--FPCPTSYRTALTYLDITNPRTNVLYELAQYASEPSEQ	399
	..*.*.*	
HsMTRR	RRLOEL--CSKOGAADYSRFVRDACACLDLLAFSPCOPPLSLLLEHLP	446
CeMTRR	RRLLEL--CSAOGMKDFIDFVRTPGLSLADMLFAFPNVKPPVDRLIELLP	450
HsCPR	ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCCELL	449
	..*.*.*	
	FAD	
HsMTRR	KLOPRPYSCASSSLFHPGKLHFVFNIVEFLSTATTEVLRKGVCTGWLALL	496
CeMTRR	RLIPRPYSMSS---YENRKARLIYSEMEFPATDGRHRSRKLATDWLNSL	497
HsCPR	RLOARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---	494
	..*.*.*	
HsMTRR	VASVLOPNIHASHEDSGKALAPKISISPRTTNSFHLP-----DDPSIP	539
CeMTRR	R-----IGDKVOVLGKEPARFRLPPLGMTKNSACKLP	529
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFK-----ATTP	527
	..*.*	
	NADPH	
HsMTRR	IIMVGPGTGIAPFIFGLQHREKLOEHPDGNFGAMW-LFFGCRHKDRDYL	588
CeMTRR	LLMVGPGTGVSVFLSFLHFLRKLKODSPSDFVDVPRVLFFGCRDSSVDAL	579
HsCPR	VIMVGPGTGVAPFIFGIQERAWLRQOGKE---VGETLLYGCRRSDEDYL	574
	*****..*.*.*	
	NADPH	
HsMTRR	FRKELRHFLKHGILTHLKVFSRDPVGEAAKPYQDNIOQLHGOOVAR	638
CeMTRR	YHSELEMFVSEGIITDLIICESEQ-----KGERVODGLRKYLDKVLP	621
HsCPR	YREELAQFHRDGALTOLNVAFSRE-----QSHKVYVOHLLKGDREHLWK	618
	..*.*.*	
	NADPH	
HsMTRR	ILLOE-NGHIIYVCGDAKNMAKDHDALVOIISKEVGVEKLEAMKTLATLK	687
CeMTRR	FLTASTESKIFICGDAKMSKDVWOCFSDIVASDOGIPDLEAKKLMOLK	671
HsCPR	LI--EGGAHIYVCGDARNMARDVONTFYDIAELGAMEHAQAVDYIKKLM	666
	..*.*.*	
	NADPH/FAD	
HsMTRR	EEKRYLODIWS	698
CeMTRR	KSDQYIEDVWG	682
HsCPR	TKGRYSLDWS	677
	..*	

FIG. 4 page 2 of 2

FIG. 5A

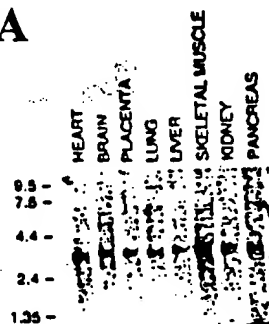


FIG. 5B





FIG. 6

FIG. 7A

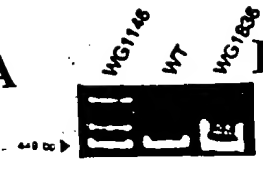


FIG. 7B

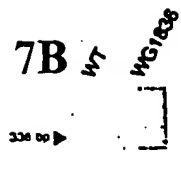


FIG. 7C

Position	Sequence	Accession/ Protein	Organism
572	CAPLLVPCWHPDQVLP	(AF025794) MTRB	[H. sapiens]
558	CTLLVYCCPSPDEDLY	(AA0557) CPR	[H. sapiens]
559	CTLLVYCCPRAEDLY	(D00101) CPR	[O. cuniculus]
560	CELLVYCCPSPDEDLY	(P31090) CPR	[D. melanogaster]
572	CPALLVPCWHPDQVLP	(P31114) CPR	[V. radiata]
573	CPVLLVYCCPSPDEDLY	(Z24438) CPR	[A. niger]
1281	CPNLLVYCCPSPDQVLP	(D14408) NOS 1	[H. sapiens]
1009	CPNLLVYCCPSPDQVLP	(U05410) NOS 11	[H. sapiens]
1040	TPNLLVYCCPSPDQVLP	(L24514) NOS 111	[H. sapiens]
100	CPNLLVYCCPSPDQVLP	(U05094) NOS	[O. cuniculus]
1009	CPNLLVYCCPSPDQVLP	(U44504) NOS	[C. gallus]
481	CPNLLVYCCPSPDQVLP	(M21004) SN	[S. cerevisiae]
915	CPNLLVYCCPSPDQVLP	(L24404) SN	[S. cerevisiae]
407	CPNLLVYCCPSPDQVLP	(Z21140) SN	[S. cerevisiae]
341	CLAVLLVYCCPSPDQVLP	(X75419) FNR	[S. sativus]
341	CLAVLLVYCCPSPDQVLP	(P00455) FNR	[S. oleracea]

FIG. 8A

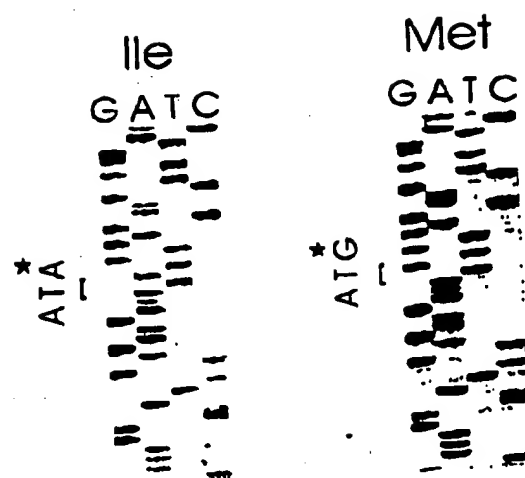


FIG. 8B

